

SEQUENCE [L1] LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: Institut National de la Santé et de la
Recherche Médicale
(B) STREET: 101 rue de Tolbiac
(C) CITY: Paris
(E) COUNTRY: FRANCE
(F) POSTAL CODE (ZIP): 75013

(ii) TITLE OF INVENTION: oligophrenin 1 gene and protein

(iii) NUMBER OF SEQUENCES: 27

(iv) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

TTTTTCAACC CATGGTGCAT TTAAAGCTCA TTTTGGACAT TTTCCCATAA ATTAACCTTA
60

AAGATAAAAA GAGTAAGAAA CAAACTTTC CCCTGAGATG TGGCTACTTA TTTATTTTCA
120

GAGGGCGTTT TCTCATGCGC ATTCTGCTAT ATAGTGTAGT GGTCAAGAGC ACTACCTCTA
180

GAGCCAGCCA GGCTGGGCTC AAGTTCAAGT GCTGCCATTT AACTAGCTGT TTGTCCTTCG
240

GCAAGTCACT TAAACTCTCT TTGACCCAGC TTCTCCATCT TTAAATGGGT ATAATAATAA
300

AACCATCCTC ATAGGGTTGT TTTGAAGATT AGTGAGATGG GCGATAGGTT GTGTGGTGGG
360

TAGAATAATG TTCCTCCTT CACAGATGTC CATGTCCTGT CCTGAAACCT GTGGCTACGT
420

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TATCTTATGT GGCAAAATGA AATTTGCAGA TGTGATTAAG GATGATGTGA TGGGGGAGAT
480

TATCCTGTGG ACCCAGTGTA ATCATAAGGG TCCTTAAGGG GAGGCATGAG AATCACAGTG
540

ATGTAGCATG AGAAAGACTT GACTGGCCAG TGCTAGCTTT AAAGACGGAG GAAGGGAGCT
600

ATGAGCCAAA GGATGTGAGC AGCTTGAGCC GGAAAAGGTA AGGAACCAGA TTCTACCCCT
660

AGACTATCTG AAAATGAACA CAACCCTTCT AACATCTTGA TTTGATCCCA GTGAGGCCCA
720

TTTCTGATTT CTGCCTTCTG GAACTGTAGA TTATACTTT ATGCTGATTT AGGACATCAA
780

GTTTGTGGTA ATTTGTCACA GCAGCAGCAA CAGGACCTAA TTCAGGTGGG TCAGCCACTA
840

TTATTCTATT TACAACCCCC TTCCGTTCTG GCTTTCTTCA CAGGGCAATC TAATGTAAAC
900

ACTTCTGCAG AATTAAAGGG ATCTCTTTGC CCACGCACAA ACTATTTTTT AGTTTTTCGA
960

GCCTCTACCT ACCCTTAGTC TCAAGACAGC TGCCTTTAAG GTAAGCTGCA AGACAATTTA
1020

TAACATCCTA TTCTTAGACT TTCCACTTAC ACATGGAAAA TCATATGCAT TATCGGCGTC
1080

TGCCACAAAA GCCATGCTCT GAGGTCCTAT TCAGGAAAAT ATTAAGTCTG AATTATGGCC
1140

TCCCTTTCTT TGGCAGGGGG CACTGAGCTT CACGGAGACC CTAGAGTAGG AATCAACCCT
1200

TCAGGTGGAA GGCCCAAGGG AATTAGAGCA CTTAGAGCAG GAGACATGGG AAAAGAAAGA
1260

GGAAAAGAAG TTGGTAGGTC CGAAGGAGGC TGGAAAGAGG GGAAGGCAAA AGAATACACA
1320

ACCCAGCCGA ATCATGGGAA GTGAGAGATG GCTTCCTGCA ATCTAGTCTT GCGGGTTCTT
1380

GCTCTAGTTT CGGAAACTTC CCCCAGCAGAG TCCAGCGCCG CGCACCTGCC CCTTGGGGCC
1440

GGTCCCTGCG CAGGAGCCTG CGGCAGGCTG GGAATGCCGT TCTGGGAGAG CAGCCTCCCA
1500

GGCGGGGTGG TGGGGAGACT GCAGGGAGGA GTTTTGGGGA GTGCAAACGG AAAGACTACA
1560

TTTCCCAGGC CGCCACGCTT TCCAGCTGGA GTCCTAGGGC GCTGACTGCT CCCAGTTTC
1620

00TCTT 224860

CGTAGGGAAG CGCTGGGCTA CCGCGGCTAT
1650

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1079 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 (A) NAME/KEY: exon 1
 (B) LOCATION: 1..634
- (ix) FEATURE:
 (A) NAME/KEY: exon 2
 (B) LOCATION: 778..935
- (ix) FEATURE:
 (A) NAME/KEY: oligonucleotide
 (B) LOCATION: 727..746
- (ix) FEATURE:
 (A) NAME/KEY: oligonucleotide
 (B) LOCATION: 958..977

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TGTGCGTCGC GCTCTCGCCC TCCTCTTCCC GCTGCAGTGT CTATGGAGCG AGGCTACGTT
60

TCATTGCCGC CCTGGCTTAA CCCTTCCGGC GCCTAAAAGG ACGGCCGGCC GGCCGGTCCC
120

TTGCACCAGG AAGAAGTCTT AGCAGCCAGC GGGCCCTGGT CAGGAAACTC TAAGGTACAA
180

GGAAAACAGT TGAGGAAGGA GCCAGAGCGC TCCGGTTTGG TCCTCGGGCT TCGCTGGGGC
240

GGGGCGCAGG CGTTGGCTTT AAGAAAGGGG AGGGGACAGT GCAATCCGGG TTGCCCCGCG
300

ATTCGGCCAA GGAATCTTCC GCTCGCTCCG GAGCGAGGAG CCTGTAAAGA GGCTGTTCCC
360

AGCTCCAGCT CTAACCTCGC CTACACCTTG GGCGGGCCCA ATGTCACGTT TGCAATTGCT
420

CAGGAAGGAT CCGGCCCGTC TCCGGAGGCA AGTCGGGCTG CGGTTTTTGC TGCTTATCTG
480

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GGAAGGCGAT GCCTAAGGGA CATGCTGCTT GCTAGGCAGC ACCCTGCCGG GATCCGACTG
540

CGATAGTTAG CTCTCCCTGG CCCTGAAGCC ATCGCCGGGG CGCCTGTTCT CTGTCCGGAC
600

CAGCCAGCGC TCCTCAGGAG TCTCACTGAA ACAGGTACCT GTCCTCCAA GGGACGGAGG
660

CTATGAGCTT CCTTAAGCGG GTCGCGCGCT CAGTCCGTCC CCTCTACTTC CTCTACTGTG
720

CCATTGATGC TCTCGGTCTT TGTGTCTTTC CCCTTTCCCC CTACTCCCGG CCATCAGAAC
780

CATGGGTCAT CCCCCGCTGG AGTTCAGCGA CTGCTACCTG GACAGCCCCG ATTTCCGCGA
840

GAGGCTCAAG TGTTATGAGC AGGAACTGGA GAGGACCAAC AAATTCATCA AAGACGTAAT
900

CAAAGACGGC AACGCGCTTA TCAGCGCTAT GAGAAGTAAG TGCAAGGCTT CGATGAGCTG
960

TTTCTCTGAN CTGGTGTGTC TGGCCTTTAA GCCTTTCCAC ACCACCAGGG GAAGGGAGAT
1020

TGCAGGGTGA CTCCCAGCCC ANATCTCTGA GGCAAATGGG TTTCCACAC TTGGGGAGT
1079

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 900 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 3
- (B) LOCATION: 403..498

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 375..394

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 504..523

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CTTTGAACTC CACACGTATA AAATGGAAAG CATCTAGTGT ATTGCCATA ATAGGGGTTT
60

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AGGAAATGTG TAAGGAGACC CTCTTAAGAG TATATCTAAG TAGTTTCATG TCTTCCATGC
120

TTTGAGTGGA ACAGGTCAGA GAGGAGAGGT GTTGAGGATA AAAACATGTC CCGTAACTTT
180

TAAGGACTTT ACTGAGATGC CCCATCCTTT CTTCTTGGA TTTAGTTGT TCAAACCTTC
240

TTCTACTGCA TATCTAATCT TTTGTTTTAT TTCATTAAAT GCTAGTTGCA ACCTGCTCAG
300

AGCACTTACC TTTGGTTTTTC TTTTATCTGC TCTTATAGAG ATGAGGAAAT AGATCAAAGC
360

ATAGCATTGT TGAACATTTT TCTTGTTACC CTCCTTTGC AGATTATTCT TCTGCTGTTT
420

AGAAATTTTC CCAGACGCTG CAGTCATTTT AGTTTGATTT CATTTGGAGAC ACTCTGACTG
480

ATGATGAAAT TAACATCGGT AAGTCTTCAG CTACATGTGG TCATATACCT GTTGAGGCAG
540

CCCTGAGACC ATGTAGTCTT TTTGATTGT GGATACAGAG CACTTGGACA TCTTCATCCA
600

CTGTGGTCCA ATGCCAAGGC CCTGGGAGGT TGATTAGGAA GGATCAGGAA ACTTTCCCTG
660

CCAGTCCCAT TTCCTCCTCA CACGACAGCA ATCAAAAGAT ACCCTTAAAC TTCTACTGAG
720

ATTTTTGACT CAGACAGTCT GCAAGCGACC TTTTCTTTAA AGCATAGTTA TTTTCCTAAA
780

GGATATATTA AAAGGGGGAC TTTTTGGTT TATTTCCCAA AATGGTTGGA GTTAGATTCT
840

TCTAAGGAAT CAAATTTCCC TAGAAAGTGT TAAATTAGCA TTTGTGTGTC TACAACCTAT
900

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 4
- (B) LOCATION: 483..544

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(ix) FEATURE:

(A) NAME/KEY: oligonucleotide
(B) LOCATION: 418..437

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide
(B) LOCATION: 551..570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TAGAAGAGTA GAAAGTTTGG GAGGGTGGAA AGGGTAATGT TTATTATTTA CTTTGTGTTG
60

ACACTACATT CACCATCCAA TTTAGTTTTT ACAGCAATAG TCTCTGGTTG GTCAGTAGTG
120

GAACAGGGAT CCAAACCTCGT TTCAGGGTTC TATAGCTGCC AATTAATTAC ACAGCAAACC
180

TCTTGCCCCCT TCCCTAATCT TTTAGCTTGT CTATGAAATA AGAGAAATTC TAGCTACTCC
240

TGAGTGGCTG TAAGGATTAA ATAAATATT AAAGTGTATG GGGATTGATA AAAGAGGAAA
300

GAAAAGAAAA GAAACATTCA ACAGGTGCTG AACACCTGCT TTTGTCCTCC GATTTGACAC
360

CTTCCTCTAG TGGCCATGTG GGCATAGGGC ACTGGTCCCT ACTTCCTGTT GCACAGATCT
420

CTATCCATTT GTCTGTCAAG CACCATGATT AATTTGTTTT ACATTGATT CTCTCCTTCC
480

AGCTGAATCC TTCAAGGAAT TTGCTGAATT GCTCAACGAG GTAGAAAATG AGAGGATGAT
540

GATGGTAAGT CACTAACGCT GTCACTGAAG CTGAGTTCAT GGGTGATATA GGGGATTTTT
600

CCTTTCCTTT ATGCTTGGAT TGATCCTATA CTATTTTGAT TTCTGTCAGA TAGCTTCTTG
660

GTGCTATAAA AATAGTTAGG TAATAGATCT GGTATTATG TCTCAAGCTT CCACCCTGAG
720

AGTTTGGCAT TAGATAGAGG GAAATTAACG TGCAAATCCC ATCTGTGTTT ATTTGAGTGA
780

AAAATAATTT CAGTGGATAT TAAACTGGGC CTTTGAACAT GTTGACAGAA ATTGAGGTCT
840

TTAGTGTTTT TAGCCAAATT ATCCATTTGT TAATCTTTAA TTTGTGGAGT AGTTTTACTT
900

TTATAGAGAA AATCAGTAGA AAATAAAGAT AGAACTCATA TACCACCTTT CTCTCTCCCA
960

09541433 412400

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 960 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 5
- (B) LOCATION: 451..522

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 423..445

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 553..574

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TCTGGTTTTA TGGCACAGGC AGGACTGTAA ATGTTTTATC CTAATGCTAT CACTGCACAC
60

TCATTGCGCT CTGATGAAAT GATTGCACT TGCTGCAATT GTCCTTTTCT TGTATTTGCC
120

ATTCTCTTTC TCTTCTCTTT TTCACCTGTC CTCAGGTCT CCTGTGTCCT CTGCTGGACA
180

TCACTTCAGA TATTTATCGA TTAAAACTC AGGTCAGACT ATCATTAAAG TTACAGAGAA
240

ATGCCCTCT TATTCTTTCT CCCATTCTT CTCAATGCAT TTGATTTTTC AGAAACAATA
300

TAGAAACAAA CAGTAACAAA ACCCAACAAA TCAGCAAACC ATTTAACATT TTGCAGGTTG
360

GTATATAAAT GAAATGTAG TAACAAGGAA TCTTGTATCT GAACCTTGTT AACCTAGAAA
420

TTGTTTTGTT TGTTTTTCCT TTTGTCTAG GTACACAATG CTAGTGATT TCTGATTAAA
480

CCCTTGAAA ATTTCCGGAA GGAACAAATA GGCTTCACCA AGGTACATTT TCTGTATATG
540

CATAAGATTT TTAAAAATAG CAATCGAATA GTTGTATGGG CTAATATTCT TCACTTTACA
600

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AAGATATGCA CCAATCTGCT GGTGCTTTGC TCTTGGCCTA GTCAGCCTCC TAAACTGTGC
660

AAAATAAATG TTTGTTGTTT ATGTCACCCT GTCTATGGCA TTCTGTTATA GTAGCCTCAG
720

CTAACATGAC AAAGGGGGTG GGGAGGTGGG TGATTAGTTT CTATGAGAAA ATGATCACGA
780

AAGAGAGTAA GAAAATCTAG AATTGGCCTC TGACTTTGTG GCCAACAGGC TCTGTATCTG
840

TGCATAAGTT TCTTCTTCTT TTGGTGTTTT TGTTGTTTTG TCTGGAAAAC TAGCTAGCTA
900

TCATGTATCA ACTGCCTGCT ATATTGAGCA CTAGGCTAGG TGCTTTACGT TCATTCTTTA
960

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 6
- (B) LOCATION: 416..517

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 388..407

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 540..559

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

CATTGTAGAT TAACCTTTTC ATGACAAATA TTTACTTCCA TTTGTGTTAT GTCTTCTTCC
60

TTTGTAAGAA AATTTGAATG AGTGGTTAAT CTATGTGAAA AATATTGGAG GGAAGAAAAT
120

ATATCTACTG CACAGGCCCT TTTAAGGTAT CATTCTCTAA GGAGCAGCTT CCATAGCTTT
180

CAGCTGTAAA AATAGGGACT GCCATTTCTG CAGGCAGAAT GGTTTGGGGT TATATTTTCAG
240

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GAAGCTGAAA CTGCTGAGAC CAATACAAAG TTAATTCTCC GTTGCTTTTT TTTCTTCCA
300

GGAGCTAGAG GGATTGACCA CCTGAAACCT GACACTATCT CCTTCATTCT CCTTTCTAAG
360

CAGACAGAGT TACAACTACA GACATTTAAT CTTTGCCCTT CTTTCCCACC TTTAGGAGCG
420

GAAAAAGAAA TTTGAAAAGG ATGGTGAGAG GTTTTATTCT TTAAGGATC GGCACCTACA
480

CCTGTCTTCA AAAAAGAAAG AATCTCAGTT ACAAGAGGTA TGTTACACAA GCCTGCCCCT
540

GCCTTCCATT GCTAGCTATG CCTTAGAAAC AGTGTGAATT TTGTACTGCA AGGCTTTTCC
600

CATACCCCGT CTCAGCAGGG AACCTCATGT GATAGTAGCA CTTGTAGTCA AACTGTGGC
660

CTGAGACTCA GAAGCCCTGA ATACTAAGCC AGCTCTTCCA CTAATCAGG GTGTGACCTT
720

GGATAGGATA CTTCTTTCTT TGCCTCATTC CATTATCTGT AAGAAGAGGA GTCGAGAGTC
780

CCTTTCAATT GCAAGTCCAA AATCCATGCG AGGATAAAGT TAAACTAGTG TTGTATTTGG
840

TAGAAATCAG GAACAGATCT TCTACTTTTT TCCCTGAGAG ATTCCACAAC CTTTTTTTTT
900

TTTTTTTTTT TTGGTGAGGG GTTAGGGGAA TGTTCTGTTT TGGGACTACT GGTTACCTGG
960

GACTTGCAGT GCCTTCAGTT CAAATAAGCT ACCATTCGGT GAGACCCTAC CACATGCCAT
1020

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1020 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 7
- (B) LOCATION: 464..574

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 436..458

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(ix) FEATURE:

(A) NAME/KEY: oligonucleotide

(B) LOCATION: 584..603

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CATTTCTTGT TAAATAAGAC TTGAGACTTG CAGTTCTTTC TGTGTGAATC CCCTCAGTAT
60

TGGCCATAGT AGCATGCTTC TGTTCCTGGG CTTTGGCCCT TGTTAATTTT TTATTCTCTG
120

TATTCATGTC TCTGTAGTGT TTGAGGGAGC AGATTTTCCT CTGACTTCAG TTCTCTGTTG
180

AATATAATAA AATGTGTGGA TTTTACACTT GTTCAGCTTT TTTCTTTTTG TCAGGGTGGA
240

TGTAATGACT TCAAGCTTTT TATGTGTTGG ACCAGAACT GGAATCCTGT ATCAGTCACT
300

TTTTTATCTC TTGGCTTTAG GTTCTCTATT TCTAAAATAA AAGGTAACAT CACTAGTTGG
360

TGGCTAAATG CTCATCTAGC TCTAGCATTC TGTTCAATCC TTAAGTACTG ACTTTCATGA
420

ATGAATATCC CAATATGTAA TGTTTGTTTT CCTTCTTCTA CAGGCAGACC TACAGGTGGA
480

CAAGGAGAGG CACAATTTTT TCGAGTCCTC TCTTGATTAT GTTTATCAAA TCCAGGAAGT
540

TCAGGAGTCC AAGAAGTTCA ATATTGTGGA GCCTGTAAGT TTTCTCTGTT GATGAATGGT
600

CTAAAAATAT TTATCAAATG CCTGGTAAAT GTACAAACTT TGATCATAAA AACAGAATCC
660

CAAAGAACGT GAAGGATAAT CAGTGGAAT GTCTAGAACG TAGTCTAACT TACGTTTTTC
720

TTGTTCTTTA GTATACTTTT TTTCTCTCTT TCCCCCAAC CCTTTTCTCT CTTTTTCTAT
780

GGCTATTTTC TTTCTCTTTC CTTTTTTTCC TTTCTCTTTC CTCCCCCTT CCGGAATTC
840

TCTACAACTC TTCCTGTTAC TTTGTTTCCC TCCCTTCCTT CTTCTTGCGC TTTCAGAAGC
900

TTCTGAAAGT CTTTCTCATA TACCAGATAC TATGCTAGGG ACTCATGTCT CTTGCAGTCA
960

GTGACTTCTC ATTCTACTAC TTTTACTTCT GTCTTGTGTA GTTTTTTCCC ATTTACGTT
1020

09581422 12-100

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 8
- (B) LOCATION: 244..348

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 219..239

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 363..381

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GCGCCACCAC GGCCAGCTAA TTTTGTATT TTTAGTAGAG ATGGGATTTC ACCATGTTGG
60

TCAGGCTGGT CTCAAACTCC TGACCTCAG ATCTGCCCGC CTCGGCCTCC CAAAGTGCAG
120

GGATTACAGG CATAAGCCAC CACACCCAGC CACACCATGG AGTTTTTTGG TGAGTTCATG
180

TTTCTTTTAT TTAGTTTATT AGAAGATGCT GGTGATAAAG TTATTTTAC ATGTTTTCCC
240

TAGGTCTTGG CCTTTCTTCA TAGTCTGTTC ATTTCTAACA GCCTGACTGT GGAGCTCACA
300

CAGGATTTCC TCCCATACAA ACAACAGCTC CAACTCAGTT TACAGAATGT GAGTTTGCAT
360

GTGGATTTTT CTCACCGGTC TTTCCATTCC GATTGAATTT CAGCCCTAGC GACCTTGATT
420

CTTGGAATTC TAGGTTACTG CATCCTAGCC AATTGTTAG AATATACTGG TGTGGATCA
479

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 600 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: exon 9

(B) LOCATION: 134..263

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide

(B) LOCATION: 108..128

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide

(B) LOCATION: 336..355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

ACCATTTCTT TTTTGTCTT GTGGTGCAC ATGCTGTAAG CAGGGAAAAC TTTGTACTGA
60

GTCTCTGACC AAGAAATACT TTTTCATGAT AATGATGATG ATAATAATGA TTTTCATGAT
120

GATGTCTTGA CAGACAAGAA ATCATTCTC CAGTACCCGG GAAGAGATGG AAGAACTTAA
180

GAAAAGGATG AAAGAAGCTC CCCAGACATG CAAACTTCCA GGACAGCCAA CTATTGAAGG
240

CTATCTCTAT ACACAAGAGA AATGTGTGTG GGGACATAGG GGTATCCATT GGGTTTCAAT
300

AAGCCAGGAA GTACTGCCAC TTGTCGGCTG TGAATTTTGG GCACCCCTTAC TGTTCATAGA
360

CCCCTGATAG CTAAAATTCC CTTGGAACGC AGGCAGGGAA TACTGAAAAC AAAAAAAAAA
420

AAAGGAGAAA CTGAGAGGAA GTTAAAGATT TGTCTTACAA AGGCTGTGTA GTGATAAGAC
480

CTAAGGTTTT CTCTGAGATT CAAAATGGGT ATTATTTGTT CTTTAATCCT TCTGATTATT
540

CTTTTGGAAA AAAGGGAAGT AGAGGAAAGG AAGTAGAAAA ATAATATTTT TTATACTTAT
600

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1020 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

09581402 12100

(A) ORGANISM: Homo sapiens

(A) NAME/KEY: exon 10

(B) LOCATION: 383..483

(A) NAME/KEY: oligonucleotide

(B) LOCATION: 361..380

(A) NAME/KEY: oligonucleotide

(B) LOCATION: 492..511

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

AGAGAGATGT GTAGAGTCAT GTACAGGTTA GAAGGGGCAT AACCCAATGA CCAATGACAT
60

GGAACAGTTA TAGAGACAGC AAAGTAAATG ACAATAGTCT CCAGCTTCTG GGATATATGG
120

TGATACAATT TATAGGGAAC ATGGCAGGGA GAGTAGGTTT TGAGCAAGCC AGAAGCAGCT
180

GTGGGAAGCA GTTGGTGAAG GTTAGAATCT CCCTGTGTGC AGTAGGTAGG TGGCTATGGA
240

AGGAGGGCGG TCAGGGCAAG GGCAGGGCTG GATCTGAAGT TTGACTCTGA AGAGCAATGT
300

GTAAATAGCT TCCATCTTAG GGTGACTTC CTATACAGCT AAAATAGTTA TTCTGTCTGC
360

TCACCTTTTAC TTGTCCTTGT AGGGGCTTTA GGAATATCCT GGGTGAAATA CTATTGCCAG
420

TATGAGAAAG AGACCAAAAC ACTGACCATG ACGCCTATGG AGCAGAAGCC AGGTGCTAAG
480

CAGGTCAGTT CTTGTTTGCA CCATATTTTT GGAAATGGAT CTATGACTGT TTCTCAGAAA
540

AGAATATATG TTGACCTAGT ATCAAATCAT CAAGTTCATC ACTGTTACGT GAGGCCATGA
600

CTTTATATGT ACACCTTGGC CTAAGTTTGA GTCAGATAGC ACTGAGTTGA GTGAAAAATT
660

TCTCTGTTGA TTAGAGCAAG CCTTTTGAAA GTGCCGGTAG TCTTTCAAAC CAGTTATTTT
720

TACAAGTGCC AGTCACATTG TACAGTCAAC TATGTAAAAA TATGGATGAA TTACTTTTAA
780

GAATGCTCTA CTCTTGGATT CTTTAAATA GCAAGTTTTA AAAATATGAA TTGAATTCCA
840

[illegible]

AAATTCCTTT TTTACAGGAG TGTGTTTATG GCCCACAGTT GGAATAACCG ATACTCACAT
900

TCTATGTACT ACTCAAATAT CTTTAAGCAG TTAATCTCTC TTTTCTGCC CTCCAAACCT
960

TCTCTCACTC CTGAAAATGA CAAGATAAAT TTAACACACT GAAAAAATA GTTACTTAC
1020

(2) INFORMATION FOR SEQ ID NO: 11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 11
- (B) LOCATION: 107..198

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 81..100

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 223..242

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

CCCTAGACCA GACGCCTTCC AAGTGACACT GAAGACACTG TAGGAAGCAG AACAGCTTC
60

TGTGTCTTTT TTTAAAAATT GCCTGTTAAT TCTTGTTTCA TATCAGGGGC CCTTGGAATT
120

AACACTGAAG TACTGTGTGA GAAGGAAGAC GGAGTCTATC GACAAGAGGT TCTGTTTTGA
180

CATAGAACT AATGAAAGGT AAGCTGTGCC GCTGTGAATT GGCAATGTCC CCACGTGCCA
240

GATGCTTAGC CTGGGTATGT CTTTTATTTT CCTCCGTCAT CCCACGTTGA TGAC
294

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double

09581432 112100

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: exon 12

(B) LOCATION: 211..289

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide

(B) LOCATION: 188..207

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide

(B) LOCATION: 300..319

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCACCCCGC CTCCATGGTT CCCAAAGTTA CTGTTCTGTA AATTGCCTAT TGTTCCTTCTT
60

GAGTAAAAGA GATTTTGAAA AATTAGTATT CTGTAAGCCT ATGCTTGTTT AGTGTGACAA
120

ACTCCAGGGC AGAGAGGGAC CCTAGATCAC AAGACTCCAT TCTCTCAGTT GAATTTTCTG
180

CTTTATACTT ACCATTTTTT TCCCCCTCAG GCCAGGAACC ATCACTCTGC AGGCCCTTTC
240

AGAAGCTAAC AGAAGGCTAT GGATGGAAGC CATGGATGGG AAAGAACCTG TAAGTTACCT
300

GAACTGGGG CAAACCTCCC CAGCATATGC CAGTGTATGA GTGCCCTCTA GTGGTATCAG
360

TGGGTCTCAN ACAATTAAAT GGTAATGGAT TGTTTAGTCT CAGTTTCTAG GCTGTAAGGA
420

ATTGTTTCCA CATCTCTTAG CAGGTAAGGC AACTGGAGTT CCAGAAAGGT TGAGGGACTT
480

TTCTGAGACC ACCC
494

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

0958442.112100

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: exon 13
(B) LOCATION: 212..245

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide
(B) LOCATION: 166..189

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide
(B) LOCATION: 259..278

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGCATGAGCC ACCACGCCTG GCCTGTTCAA GTATTTTCTA GCAATCTTGG CAAAGCAATT
60

ATGTTTAGCC CACTTGGCTA TCTTTTAAAC ATCCTGGAGT TTCTAATCAT TTTTAATGCC
120

TATCTGGGGA AAGATATTTA ATATTATGTT CTCTGTTTTT CTATATTGAT TGACAATAGC
180

CATGGATCTT TCTGTTTATC TTCTTTTGTA GATCTACCAC AGCCCTATAA CAAAACAGCA
240

AGAAAGTGAG TCACTTAAGT TTTTGGTCTA CTAGCATTAT AACTGCCAG CTGTCCGATT
300

CATAGTAAAT ACCATCATTA ATGATGTGTA CTACTAACGC AAGTCTGAAT ATGGATGCCT
360

TTGTGTGAAA TAAAATTC
378

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 393 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(ix) FEATURE:

(A) NAME/KEY: exon 14
(B) LOCATION: 172..234

(ix) FEATURE:

(A) NAME/KEY: oligonucleotide
(B) LOCATION: 133..152

(ix) FEATURE:

09561422-112100

- (A) NAME/KEY: oligonucleotide
(B) LOCATION: 250..269

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

AAAATGTAA ACCTCCCCTG AAAAAATGAC TCTTCCATT TAAGGGTGAC TAGAAATGAG
60
CAACTAAAAA CCCTTAGCTC TCTCAATGCA GTCCCTTTGC ATGGTCATTA AATGTTTAAT
120
AGGTGACACC TGTTCAGCA GGATCTAACT CTTTTCCTTT GCTTGAAACA GTGGAGCTAA
180
ATGAAGTGGG CTTCAAGTTT GTCAGGAAGT GCATCAATAT TATTGAGACC AAAGGTAAGA
240
TCTGAACCAT AGTCTTGGCA TTGTCTGAAT CTCGTCCTC TGATTTTATC CTGGGCAATT
300
TCTCTGAAGT AGCGTTTTAG GAATGAAGAC TGTTTATAAA GCTTGTGTAG TAGATGCAAG
360
CTAGAAAATT TCAGAAAATT CTAACTAGT GGT
393

(2) INFORMATION FOR SEQ ID NO: 15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 436 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 15
(B) LOCATION: 207..281

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
(B) LOCATION: 151..170

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
(B) LOCATION: 293..315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

AGATTAATGA GGGTTTGGTA CACTCCAAAT GAAAGGATGG ATAATTTGGA GAGATGCTGT
60
AGGACTATTC CCCTGTTACA GGAAGGCTG GAGAACTTGG AGTATGTAGT GTGACCCCTT
120

09581423.112100

CCTATCTGAA TTGACTCTAG TGTACCAAGG GGAGATGACA ACTTTAGCTA TACAAGTGAA
180

ATTAACCTGA TTTTTCCTC CACTAGGGAT CAAGACAGAA GGGTTGTACC GCACTGTGGG
240

CAGCAATATT CAGGTCAGA AGCTGCTGAA TGCCTTTTTT GGTAACAATT TCACTTTGAT
300

AATTCCTTATT GGGAGTACTT TATGTGTTAC AAAGAAATGT GACTGGAAGA GAAAGGAGAC
360

ACTGCTAAAA TGTGCTAGAA TAGTTGAAAA AAGTATTTTC TAAAGTAAAA CATACACATA
420

CTTGCCCACC CTGGGC
436

(2) INFORMATION FOR SEQ ID NO: 16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 16
- (B) LOCATION: 270..354

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 221..244

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 363..382

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

ACCCAGTNA TNTGATGAAT CTAAGAAGAG TNGATNTTGT TTGTTCAAGT TTTTCTTGTT
60

GTGTGAATTG GATAGATTAC TTTNTTATTT CTTATATGGC AGACCAGAAT GCAGTCATGT
120

TTTTGAAATA TCAAAGATTT GCTTCTTCTA AAGTTTTGAT NTCTTAAAAA CTACTTAGGG
180

TNATATACTT TGTTTTTCTT TTAAAAGAGG GAAAATGTAA GATTTTTTTG ATGATTAAC
240

095442.442400

GAAGCAT
547

(2) INFORMATION FOR SEQ ID NO: 17:

- (A) LENGTH: 601 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

- (ix) FEATURE:

- (A) NAME/KEY: exon 17
(B) LOCATION: 355..413

- (ix) FEATURE:

- ```
(A) NAME/KEY: oligonucleotide
(B) LOCATION: 305..324
```

- (ix) FEATURE:

- ```
(A) NAME/KEY: oligonucleotide
(B) LOCATION: 438..457
```

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TAATCCCCT AAGCTGTAGG GCTCAGGAAC TTCAGCCTTG CTGTCCCCAG AACTAAGAAT
300

CCAATACCCA GCTGCTTTNT TCCCAAAGCA ACTGACAATT TTCATTCATT TCAGGAATCT
360

TTCTGAACCT GTCATGACCT ATAGACTTCA CAAAGAGCTG GTCTCTGCTG CCAGTAAGTA
420

TTTATGTTAC TAATTAAGTG TGTGTCCTA GTTCTTAAT GTTACTGCA ATAAGCCTAG
480

AAAATTGTTT GAGGGGAAGT GATTGAGGGC ACAGAAACCT AAAACACATA CACAAATTAT
540

GCACAAGTGC CAAATGAAAG TATTCTTGCT TGCTGTCTAA CTCAANAATT CTATTATTTT
600

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601

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 387 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 18
- (B) LOCATION: 80..185

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 25..44

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 218..237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GTGCATATAT ATGTGAGAAT TTTGCTCAAT CCAGTAGCCC AGAAAGCCAA ACCATTTATC
60

TCTTACTGTT CTATCCCAGA GTCTGACAAC CTGGATTACC GCCTAGGAGC TATTCACTCC
120

CTGGTATATA AGCTACCAGA AAAGAACCGA GAGATGCTGG AACTTCTGAT AAGACACTTG
180

GTCAAGTAAG TAACTGCTGG ATTTTCAGAA AAAGTTCCTA TTAGAGGACT GGCCCATGTG
240

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GAGTCATCAT GCATGTGGAT TGTCTCA
387

TAAGCTTATA ACTATATTAT TTTCAGACAC CATGCTAAAT
460

[illegible]

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 20
- (B) LOCATION: 230..377

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 206..225

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 383..402

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

TCTTCCAAAC TGAGAAGTGC CAGGTTNTGT GCCTTGAGCA TAGTAGGAGN TACNTAAACA
60

TTTACCTGTA GNTAGAGTGA TTAAGAAAAT CTCTGATTCT TTGAGTCATG TTAGTATTCA
120

CGTNACAAAC TCTAGATATA AGGCCAACAA GCATCAANTG GTGGGTAGCA TTCAGAAGAC
180

AAAAANTTGA TNTAANTATT CTNTAGATAT NTTCTTCTT TNTCCACAGA TCTATTTAGG
240

TCCACCTGAG GAAAGCGCTG CACCGCCAGT GCCTCCGCCT CGGGTGACAG CAAGAAGGCA
300

CAAACCAATC ACGATTTCAA AGCGCTTGCT GCGAGAAAGG ACGGTTTTCT ATACTTCTTC
360

CCTGGATGAA AGCGAAGGTC AGTACTNAGG TTCTCCTTTA GCTTCTGAAT GGTGATTAGA
420

CACNNAGNAN GATATCNAAT GGCTCAAGCG GTGGCATCAC CATTTNTCTC TCTATAAAAG
480

TANACCTTTC CTGNCTCCTG AACTTAAAAG CA
512

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 841 base pairs

09504439.112100

(ii) MOLECULE TYPE: DNA (genomic)

(A) ORGANISM: Homo sapiens

(A) NAME/KEY: exon 21

(B) LOCATION: 185..508

(A) NAME/KEY: oligonucleotide

(B) LOCATION: 151..170

(A) NAME/KEY: oligonucleotide

(B) LOCATION: 511..530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGCTTTACAT GAACTGGGAA GGGTAGAGAA TGATTTTGTG GGATATAGTT GGTTCGTGCC
60

ACAGTGACAT AACTGCTTTG AAAATGTATA CAAATTTTCA AAATTAAGTA TGTATGCATG
120

TATCAAATG AAAAGGTTTT AAAAGTTATC ATTAATCTTC CCTNTTGGCA CCAACTTTTT
180

CTAGATGAAA TCCAACATCA AACACCGAAT GGTACTATCA CCAGCAGCAT AGAACCCCCC
240

AAGCCACCAC AACACCCCAA ACTACCTATT CAGAGGAGTG GGGAAACTGA TCCTGGGAGG
300

AAGTCCCCAA GCAGGCCTAT TTTGGATGGC AAGTTGGAGC CCTGCCCAGA GGTGGACGTG
360

GGGAAGTTGG TGTCTAGGCT GCAGGATGGA GGGACCAAGA TCACCCCAA GGCCACCAAT
420

GGACCCATGC CAGGCTCTGG GCCCACCAG ACCCCCTCTT TCCACATAAA GAGACCAGCT
480

CCCCGGCCCC TGGCCACCA CAAGGAGGGT AAGTGCTTGG GAATCCCATG GGAGCCAGAG
540

CTGACCTTAA CTAAGTTTCA CCTTGAGATC CTTCTGAGTT TGGAGATATA TTTAAGTGGA
600

AATATGTTCC AGTTTACTAC CACTAATATT GGAACAGTGG GCAAGATCAC AATAATCAGT
660

CACAATAATC ACTAGAATGT AAGCTCCATG AGGGCCGGGA TTTTTCACCT GTTTTGTTGA
720

CCTCTATATC CCAAGTGCTA TGTGCCTGGC ACTGTACTAA TTGCTGATAT ACTATTTCTT
780

ATCCTCACAA TCCCACTGTA AAGAATGTAT TATTCTTAAT ATTTTCTTTT TTTTTTTTTT
840

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841

(2) INFORMATION FOR SEQ ID NO: 22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 615 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 22
- (B) LOCATION: 320..485

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 294..313

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 496..515

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

TTTAATCCTC CCACTATCTC TGTAAGATAA TATATTGTGG ATCTTTATTA TATAGCTGGG
60

GAAACTGAGA CTTAGGGAAT GGATATGACA CACCCAAGAT ATNTGAACT CCAGAGCTGG
120

GGTTCAAATA TAGACTTTCT GAAGGGACAG TTGCCAGAAA AATTACAAAA AAAAAAAAAA
180

ATAGCCAGAG TTGTTAGTCA CCAAGAAGAA ATGGAGGCCA AGGAAGTTGG CCCAGGTAAC
240

TCTCATATTG GGTGCCTGCT CATGAGTAGT GTTCTGTTTG GCTAACCATC CAAGTTCCTG
300

GTATCATTTT CTCTTCCAGG GGATGCTGAC AGTTTCAGCA AAGTGCGGCC TCCAGGAGAA
360

AAGCCAACCA TCATCCGCCC CCCAGTGAGG CCCCAGATC CTCCCTGCCG GGCAGCTACT
420

CCCCAAAAGC CAGAACCAAA GCCAGATATT GTGGCTGGCA ATGCGGGGGA AATCACATCA
480

00111 22111 33111 44111 55111 66111 77111 88111 99111

TCTGTGTCAG TAGGGTTGTA CCTCAAAGTT GACTGAAGTC CTGTACTAGG CCACTAGGAA
540

TGCTTTTCAGG ATCACCATAT TAAGGGTATA CAGTGCACAG CCCTGGGGCA TCCTTCACTT
600

TATAGTCTAG GGAAA
615

(2) INFORMATION FOR SEQ ID NO: 23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 475 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 23
- (B) LOCATION: 211..261

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 179..198

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 271..291

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AATGGGGATA AAGAGTGTC GCTATGGCCT TAGGGGTGCC TATGGGCTCT GGGCCATTTC
60

ACATTTGTAT GTGTAGGGCC TTTGCCAGCA AAGGCAGGGG CTGGCATTGG TGTCCCATCT
120

GGTTCAGAGT CTCCTGTCCT TTCTGTTGGC CATTGGTTCT CACGTGTATA CCAAAGCAAC
180

TTATGGGACT TGTTGGCTT CTGTTTGCAG GGTGGCTTCC AGGACCAGGT TTTTGAAC
240

AGCTTCCCGG AAAACAGGAA GGTAAGATAT GGAGGTGACA AAAGAAAAAC CAAATCGCCT
300

TTTAATAACT GCATCCTTAG CATACAATTG TGCTCACTCT AACATCTTTC TCTTTTGT
360

TCTCTACAGC TCTGTCTCTG TCTGTCACTT TCTCTTCCCC AATTCTGTCT CTCCATCCCT
420

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ATCTGTCTGT CACCTGTTCA CCTGTGTGTC TATTTGTTTC TCTCATATTC TTTT
475

(2) INFORMATION FOR SEQ ID NO: 24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 238 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 24
- (B) LOCATION: 115..156

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 65..84

(ix) FEATURE:

- (A) NAME/KEY: oligonucleotide
- (B) LOCATION: 165..184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CCATTTTTC AATGGCCTCT TTAGCACTGG CCTAGAAGTG TCCCCCATTC CCCCAATTTA
60

CCTTTCCAGT CCGATTCTCT AGAATCTTAG TGAAACGTCT TTCTTTATCC ACAGTTCTCA
120

AGGCAGACTT CCGGAGATG AAAGTTGAGG CTACAGGTAT GCAGTCCCCA TCCCTGATTA
180

CAAAATCTTG TTCCACATAA GCCTTCATTA CGGGATCTGA TATTTTGAGG ACTGGAAT
238

(2) INFORMATION FOR SEQ ID NO: 25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4504 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(ix) FEATURE:

- (A) NAME/KEY: exon 25
- (B) LOCATION: 1..4235

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001211-22478560

(ix) FEATURE:

(A) NAME/KEY: polyA_site

(B) LOCATION: 4236..4241

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

GTTTTAAAAG CCTTGGCCTC AGAGGACCCT TTCCAGGTTC TGAAAGAGTC TTTCTTCTTC
60

AAACCTTTGT GTGCGGAGTC ATTTTGTGTT GAAGAGCAGC TCCTTCCTAG CCTTGCACTT
120

TCAGACTCTC TCTGGGAGGC CATAAAATAA GGAGCATATG TCCTAGACAG GTGTTTATAT
180

CTCCTTTGTA TTCTGTCTTC ATCCCCTCAG AAGGTCTGTT TTGAGTTCCT ATAACACTGT
240

GAAGAGCTGG ACTCCCTCAA GCCAGACTCT GCCAAAACCA AGATATCCAC TTACCTGAGT
300

TGAAGAGGGG AGCTCAGTTT TCAACTCTTC CCTGAACTTC CTGCTTCCTC AGAGGGCCAT
360

TGAACTCTGA GAGATTTGGG GCTAAAGACT GATCTCAGGG GTCTTACCTT GAACTGAAGG
420

CCACTTGAGT TGGGGCCATT GCTTACCTTG GTTGAAGGG AATAGAAATG TTTGCTGAAC
480

ATTGGAGAAT CTCAACATGT CTCCTACTGA GGATATGGAC ACTGGTGCCA TGTCAGCGCT
540

CTGGTGCTGC AGTATGTTGC CAAGAGCCCG TCTGCTCCTG CGAGGCTATG AGTGGGATGA
600

GTGATGCCCC CACAGCACCT CCATGTGGAC TTAGGAAGGT GGCCTTCCTG CTGTTACATG
660

CAGCCACTTA GGACAAATCT GCAAAGCATG TTTTGCATGT AAAAGCCTAG GTCTATTTGG
720

ATTATTCTTT CTCCTTTTTT TTGACAGCTT CCTGTCAAGC AATCAAGAAA CAAACAAAAG
780

CTGAACACAT TTCCTTTTAA AAAAAGGAGA CTGTGTTTGG TCCTGTAGGA GTTCTATTTT
840

GGGGTCAAAT GCTAGAAAAA TTGTTAAGGT GGATTGAGGC CAGGCAGCTG TCACTGCTGC
900

TTCATGTTTG CCTTCTGCAC ATAAACTCTT TTATCTCCTG AAAAAAGCAG TTCTTAACCC
960

AGTGTCCATG GACTCAGAAA CTCCATGATG CCCCTGAGAT GGTATGCACA ATTCCATGAC
1020

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AATATGCCCT TTCTGGGGAG ATAGTCCATA ATGTTCTGCT AAATTTCAAA TGGGCTCGTG
1080

ACCCAAAAA GTCAAGAACC ACAGCACTTG AGTTAAAATA CTCTTTTAC AATCCATATA
1140

AGCCCTTGAT TGAAGGGCT TTTCAAATC ATTTAGTCTA ACAACTGCCC AGTTTCCAGT
1200

CGGGGAACT GAGGCAGAGC AAGGTAGTGA TCACACCAGT ACAAGATTTC AGGTCCCAGG
1260

CTCCTATGCA AGTTTTTTTT CCCATTATA TCACACTTAT TTAGCAAGGG ACCTTGTTGGT
1320

TTGTGGCTTT AGTGGCCATC ATTTCTGGGG GTTGGCTTTT ACCCTTTTTC TTGAATATTT
1380

GCCACCAAGT GAAAAATGTT AGGACATAAA CCCTTGCCAG GTCCCTTTCA TTTGCTATCT
1440

CTATTATTGG AAAGGACCTA AAAATTGGTG TAATGGGGCA GAAATCTGAG GAATGGACAT
1500

TTCTAATTCC TGTTTGTGA AGGGAAGTTG CTGGAAAGAG CATCAGTACT TGTTTCTATG
1560

CAGATGCCTG GGCCGTAGCT TGTCTGTAGC GTCTGTATAA TTATAATGTT GCCCAGTGTG
1620

AGGGAAAGAG CTTTCCTACT TGCACTCTTC TACCAAGGCC CTGTTAGTGC ACTGATTATA
1680

GTACTGACAG ATAAAGCCTA GATGAGAGAG ATAGAGAGTG AGTACATGCA CACTCATGTG
1740

CAAACCCACT CAGAGATGCA TTTGGAACAG TGCTACTGAA AGGCAGTAGT CATTTTCAAG
1800

ACTGAATTCC AAACATGGTT TATTGGTGAG TTAGGAACAT GTAAGGCCAA GTACACTGAG
1860

AGCCTTTTTG AAAGTAATTG AGTGGAAGT TGATGCCATT CTAAATCAAG GCATATCCAG
1920

GTGGCCCGGT TTGAACTCAC TCCACTGTAC CCAGTCTCAA AGGCCAGGTT GCTAAGAAAC
1980

CAGGAGTAAA AGAGTCAAGT GACCATCATT TCACCTGCTG CTTGCCCCCA ATAGTAGTCT
2040

CTGTGAGGCC TTAGTGACCT CACCTAGGAA GTGATTTTTG AGCCCTTGTT TCAGGGCTGT
2100

GGCCTCCCTG CTCTATCCTG AATAAAGCAG ACAGGTGTGC AGATTTTGGC CATGAAAGCA
2160

TGGCTAATAG GGCCACAGTC CCTTTAAAGA AACATGGTTT GACTCTGGTT TTCTTGGGGG
2220

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AAAATACCAC AATCACCGAT GCAAACATTG GAAGATTATT GAGAGCCCTA GAAAGCTGCT
2280

GTGATCCCAG TAGAAAATAT GTCCCAGAAA TGTCATGAGA TTGCTGTGTG TTGCCTGGGA
2340

CACAGATCAA GGGCCTATCT TGGAGAGCTG GGGACCAGCA GTCTGCCTGG AGGCCAGGGA
2400

GCAGTGGCTG AGTAGCTCTG CCTTTGCTCT GGTCTATAACC TTAAGAATGC CAAAGAATGA
2460

ATTTCAACGC CTGCCTTTGG CACTCTGACT TAAAGTGCAA AAAGCTTCTG TGGCGAGGCA
2520

TGCTATCATG GAATGAGACT GGCTTGCCCT AGGCTTAATG GATGGGCAGT CATTTTGCAG
2580

AGGCTATGGG AAGAGGGTGA TAATAGAAGA GTGGCAGCTA TAGGAAATTA TCAACATACC
2640

TTGGCCAGCA AGTTAGAGAA TCTGGCAATG GATGAACTGA AAGTGATGAA CTGGCAGGGA
2700

TAACAAAGAA CCTAACATTT ATTAAGCACG TATTTATTAA CTGCTCAGTG TTTCATATTC
2760

ATGCAAGTAT TCTCATTTTA CAGAGAAAGA AATTATGGCC CAGGGGGCTA AAGTAAACAA
2820

CTCAAGGGCA CATAGAAAGT AAATAAAAGG ACTGTGATTT GAATCCAGGC CACTCTTAGC
2880

CCATGCTGTT TTCCCTTTGC CACACTGTGG TAGGTGTTTG AACAGAGGCC ACATTACTAG
2940

AGTTGGCATG ACTCTTGACT CTTGCCTGCC TAACAAAATA TTGAAAGGCA AACATTTGAA
3000

GGAGGGAGGG GGTGCAGGTT CAGTTTATAT GGAAATGCAA ACTGGGCTGG AAGATATTCC
3060

TGAGTTAGGC TTTCTCTTCA TATTCAGCTT GCACATTTGG TAATGTTTTT AAAATGATCA
3120

TCTAATTTTA TTTTGTGAAG TGAAGGATTT GTGTTTTAGT TGGCAGTTGT TAAGTCCTTG
3180

GCTTGCCATT TTTCAAAAG TAAAAAGGTC CTCACAGGTG TCTCCATACT TCGCCAAGGT
3240

TGTAGCATGG GCAGTTTCAG TTTCAGCCTA AGAGACTGGT GACATCCACA AATGCAGTTT
3300

TAGAAGCAGA AAAGGTCTTG GTGCCTCTGC AGTACTTGAT GTATTGGGGT CAAATCTCTA
3360

CAAATTTTTT TGTGGTGATA GCAAATCAA GAGATGGCTT ACAAAAAGAA ATATTGAATT
3420

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TTTATTTTGT AAGTTTTTGT TTTTAAAAG GTTGGGGGTG TTCAGCCACT GAGGGACAAA
3480

ACTTAGCATC TAATTTCAAT TATAGTGTC TGCAGAGTAT TTCTAAAGTA ATTGGTTATC
3540

ATGGGAAAGT ATTCTCTTTT CAAGAAGTTC TTTGATTCTG TAATAACTAG AACAAATAAA
3600

GTAGTAAAAG AAGAAATAGT TCTGTGACTA GGAAAAAATT GCTTTTGAGA GAACATAGAT
3660

CAATTATACT ACTTCTAAGG TAGCTGCAGA TAAGTGGCCT TGACACATTA CAAGCCTGGA
3720

AAAAAACATC AGAAATAATA AAAAATTTCA GAGAGAATCA AGATACCTTT TTTTTTCTTT
3780

TTTTTTTCTT TTTTTTATTA TACTCTAAGT TTTAGGGTAC ATGTGCACAT TGTGCAGGTT
3840

AGTTACATAT GTATACATGT GCCATGCTGG TGCCTGCAC CCACTAATGT GTCATCTAGC
3900

ATTAGGTATA TCTCCCAGTG CTATCCCTCC CCCCTCCCC GACCCACCA CAGTCCCCAG
3960

AGTGTGATAT TCCCCTTCCT GTGTCCATGT GATCTCATTG TTCAATTCCC ACCTATGAGT
4020

GAGAATATGC GGTGTTTGGT TTTTTGTTCT TGCATAGTT TACTGAGAAT GATGGTTTCC
4080

AATTTTCATCC ATGTCCCTAC AAAGGATATG AACTCATCAT TTTTATGGC TGCATAGTAT
4140

TCCATGGTGT ATATGTGCCA CATTTTCTTA ATCCAGTCTA TCATTGTTGG ACATTGGGGT
4200

TGGTTCCAAG TCTTTGCTAT TGTGAATAGT GCCGCAATAA ACATACGTGT GCATGTGTCT
4260

TTATAGCAGC ATGATTTATA CTCATTGGG TATATACCCA GTAATGGGAT GGCTGGGTCA
4320

AATGGTATTT CTAGTTCTAG ATCCCTGAGG AATCGCCACA CTGACTTCCA CAATGGTTGA
4380

ACTAGTTTAC AGTCCAACCA ACAGTGTAAG AGTGTTCTTA TTTCTCCGCA TCCTCTCCAG
4440

CACCTGTTGT TTCCTGACTT TTTAATGATT GCCATTCTAA CTGGTGTGTA GATGATATCT
4500

CATA
4504

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3101 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
- (ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 639..3047
- (ix) FEATURE:
 (A) NAME/KEY: oligonucleotide
 (B) LOCATION: 152..172
- (ix) FEATURE:
 (A) NAME/KEY: oligonucleotide
 (B) LOCATION: 586..606
- (ix) FEATURE:
 (A) NAME/KEY: oligonucleotide
 (B) LOCATION: 641..663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

TGTGCGTCGC GCTCTCGCCC TCCTCTTCCC GCTGCAGTGT CTATGGAGCG AGGCTACGTT
60

TCATTGCCGC CCTGGCTTAA CCCTTCCGGC GCCTAAAAGG ACGGCCGGCC GGCCGGTCCC
120

TTGCACCAGG AAGAAGTCTT AGCAGCCAGC GGGCCCTGGT CAGGAAACTC TAAGGTACAA
180

GGAAAACAGT TGAGGAAGGA GCCAGAGCGC TCCGGTTTGG TCCTCGGGCT TCGCTGGGGC
240

GGGGCGCAGG CGTTGGCTTT AAGAAAGGGG AGGGGACAGT GCAATCCGGG TTGCCC GCGG
300

ATTCGGCCAA GGAATCTTCC GCTCGCTCCG GAGCGAGGAG CCTGTAAAGA GGCTGTTCCC
360

AGCTCCAGCT CTAACCTCGC CTACACCTTG GCGGGGCCCA ATGTCACGTT TGCAATTGCT
420

CAGGAAGGAT CCGGCCCGTC TCCGGAGGCA AGTCGGGCTG CGGTTTTTGC TGCTTATCTG
480

GGAAGGCGAT GCCTAAGGGA CATGCTGCTT GCTAGGCAGC ACCCTGCCGG GATCCGACTG
540

CGATAGTTAG CTCTCCCTGG CCCTGAAGCC ATCGCCGGGG CGCCTGTTCT CTGTCCGGAC
600

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CAGCCAGCGC TCCTCAGGAG TCTCACTGAA ACAGAACCAT GGGTCATCCC CCGCTGGAGT
660

TCAGCGACTG CTACCTGGAC AGCCCCGATT TCCGCGAGAG GCTCAAGTGT TATGAGCAGG
720

AACTGGAGAG GACCAACAAA TTCATCAAAG ACGTAATCAA AGACGGCAAC GCGCTTATCA
780

GCGCTATGAG AAATTATTCT TCTGCTGTTT AGAAATTTTC CCAGACGCTG CAGTCATTTT
840

AGTTTGATTT CATTGGAGAC ACTCTGACTG ATGATGAAAT TAACATCGCT GAATCCTTCA
900

AGGAATTTGC TGAATGCTC AACGAGGTAG AAAATGAGAG GATGATGATG GTACACAATG
960

CTAGTGATTT GCTGATTAAA CCCTTGGAAT ATTTCCGGAA GGAACAAATA GGCTTCACCA
1020

AGGAGCGGAA AAAGAAATTT GAAAAGGATG GTGAGAGGTT TTATTCTTTA CTGGATCGGC
1080

ACTTACACCT GTCTTCAAAA AAGAAAGAAT CTCAGTTACA AGAGGCAGAC CTACAGGTGG
1140

ACAAGGAGAG GCACAATTTT TTCGAGTCCT CTCTTGATTA TGTTTATCAA ATCCAGGAAG
1200

TTCAGGAGTC CAAGAAGTTC AATATTGTGG AGCCTGTCTT GGCCTTTCTT CATAGTCTGT
1260

TCATTTCTAA CAGCCTGACT GTGGAGCTCA CACAGGATTT CCTCCCATAC AAACAACAGC
1320

TCCAACCTCAG TTTACAGAAT ACAAGAAATC ATTTCTCCAG TACCCGGGAA GAGATGGAAG
1380

AACTTAAGAA AAGGATGAAA GAAGCTCCCC AGACATGCAA ACTTCCAGGA CAGCCAACTA
1440

TTGAAGGCTA TCTCTATACA CAAGAGAAAT GGGCTTTAGG AATATCCTGG GTGAAATACT
1500

ATTGCCAGTA TGAGAAAGAG ACCAAAACAC TGACCATGAC GCCTATGGAG CAGAAGCCAG
1560

GTGCTAAGCA GGGGCCCTTG GACTTAACAC TGAAGTACTG TGTGAGAAGG AAGACGGAGT
1620

CTATCGACAA GAGGTTCTGT TTTGACATAG AAATAATGA AAGGCCAGGA ACCATCACTC
1680

TGCAGGCCCT TTCAGAAGCT AACAGAAGGC TATGGATGGA AGCCATGGAT GGGAAAGAAC
1740

CTATCTACCA CAGCCCTATA ACAAACAGC AAGAAATGGA GCTAAATGAA GTGGGCTTCA
1800

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AGTTTGTCTAG GAAGTGCATC AATATTATTG AGACCAAAGG GATCAAGACA GAAGGGTTGT
1860

ACCGCACTGT GGGCAGCAAT ATTCAGGTTT AGAAGCTGCT GAATGCCTTT TTTGATCCTA
1920

AATGCCCAGG AGATGTTGAT TTTCATAATA GTGACTGGGA CATTAGACA ATCACCAGCT
1980

CCTTGAAATT CTACCTCAGG AATCTTTCTG AACCTGTCAT GACCTATAGA CTTCACAAAG
2040

AGCTGGTCTC TGCTGCCAAG TCTGACAACC TGGATTACCG CCTAGGAGCT ATTCACTCCC
2100

TGGTATATAA GCTACCAGAA AAGAACCGAG AGATGCTGGA ACTTCTGATA AGACACTTGG
2160

TCAATGTGTG TGAGCACAGC AAAGAGAATC TTATGACCCC CTCCAACATG GGAGTAATCT
2220

TTGGGCCCCAC CCTGATGAGA GCTCAGGAGG AACTGTGGC CGCCATGATG AACATCAAAT
2280

TCCAGAACAT AGTGGTGGAA ATACTAATCG AGCACTTTGG CAAGATCTAT TTAGGTCCAC
2340

CTGAGGAAAG CGCTGCACCG CCAGTGCCTC CGCCTCGGGT GACAGCAAGA AGGCACAAAC
2400

CAATCACGAT TTCAAAGCGC TTGCTGCGAG AAAGGACGGT TTTCTATACT TCTTCCCTGG
2460

ATGAAAGCGA AGATGAAATC CAACATCAAA CACCGAATGG TACTATCACC AGCAGCATAG
2520

AACCCCCCAA GCCACCACAA CACCCCAAAC TACCTATTCA GAGGAGTGGG GAAACTGATC
2580

CTGGGAGGAA GTCCCCAAGC AGGCCTATTT TGGATGGCAA GTTGGAGCCC TGCCAGAGG
2640

TGGACGTGGG GAAGTTGGTG TCTAGGCTGC AGGATGGAGG GACCAAGATC ACCCCAAAGG
2700

CCACCAATGG ACCCATGCCA GGCTCTGGGC CCACCAAGAC CCCCTCTTTC CACATAAAGA
2760

GACCAGCTCC CCGGCCCTG GCCCACCACA AGGAGGGGGA TGCTGACAGT TTCAGCAAAG
2820

TGCGGCCTCC AGGAGAAAAG CCAACCATCA TCCGCCCCC AGTGAGGCCC CCAGATCCTC
2880

CCTGCCGGGC AGCTACTCCC CAAAAGCCAG AACCAAAGCC AGATATTGTG GCTGGCAATG
2940

CGGGGGAAAT CACATCATCT GTGGTGGCTT CCAGGACCAG GTTTTTTGAA ACAGCTTCCC
3000

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GGAAAACAGG AAGTTCTCAA GGCAGACTTC CTGGAGATGA AAGTTGAGGC TACAGGTTTT
3060

AAAAGCCTTG GCCTCAGAGG ACCCTTTCCA GGTTCGAAA G
3101

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Met	Gly	His	Pro	Pro	Leu	Glu	Phe	Ser	Asp	Cys	Tyr	Leu	Asp	Ser	Pro	1	5	10	15
Asp	Phe	Arg	Glu	Arg	Leu	Lys	Cys	Tyr	Glu	Gln	Glu	Leu	Glu	Arg	Thr	20	25	30	
Asn	Lys	Phe	Ile	Lys	Asp	Val	Ile	Lys	Asp	Gly	Asn	Ala	Leu	Ile	Ser	35	40	45	
Ala	Met	Arg	Asn	Tyr	Ser	Ser	Ala	Val	Gln	Lys	Phe	Ser	Gln	Thr	Leu	50	55	60	
Gln	Ser	Phe	Gln	Phe	Asp	Phe	Ile	Gly	Asp	Thr	Leu	Thr	Asp	Asp	Glu	65	70	75	80
Ile	Asn	Ile	Ala	Glu	Ser	Phe	Lys	Glu	Phe	Ala	Glu	Leu	Leu	Asn	Glu	85	90	95	
Val	Glu	Asn	Glu	Arg	Met	Met	Met	Val	His	Asn	Ala	Ser	Asp	Leu	Leu	100	105	110	
Ile	Lys	Pro	Leu	Glu	Asn	Phe	Arg	Lys	Glu	Gln	Ile	Gly	Phe	Thr	Lys	115	120	125	
Glu	Arg	Lys	Lys	Lys	Phe	Glu	Lys	Asp	Gly	Glu	Arg	Phe	Tyr	Ser	Leu	130	135	140	
Leu	Asp	Arg	His	Leu	His	Leu	Ser	Ser	Lys	Lys	Lys	Glu	Ser	Gln	Leu	145	150	155	160
Gln	Glu	Ala	Asp	Leu	Gln	Val	Asp	Lys	Glu	Arg	His	Asn	Phe	Phe	Glu	165	170	175	
Ser	Ser	Leu	Asp	Tyr	Val	Tyr	Gln	Ile	Gln	Glu	Val	Gln	Glu	Ser	Lys	180	185	190	

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Lys Phe Asn Ile Val Glu Pro Val Leu Ala Phe Leu His Ser Leu Phe
 195 200 205
 Ile Ser Asn Ser Leu Thr Val Glu Leu Thr Gln Asp Phe Leu Pro Tyr
 210 215 220
 Lys Gln Gln Leu Gln Leu Ser Leu Gln Asn Thr Arg Asn His Phe Ser
 225 230 235 240
 Ser Thr Arg Glu Glu Met Glu Glu Leu Lys Lys Arg Met Lys Glu Ala
 245 250 255
 Pro Gln Thr Cys Lys Leu Pro Gly Gln Pro Thr Ile Glu Gly Tyr Leu
 260 265 270
 Tyr Thr Gln Glu Lys Trp Ala Leu Gly Ile Ser Trp Val Lys Tyr Tyr
 275 280 285
 Cys Gln Tyr Glu Lys Glu Thr Lys Thr Leu Thr Met Thr Pro Met Glu
 290 295 300
 Gln Lys Pro Gly Ala Lys Gln Gly Pro Leu Asp Leu Thr Leu Lys Tyr
 305 310 315 320
 Cys Val Arg Arg Lys Thr Glu Ser Ile Asp Lys Arg Phe Cys Phe Asp
 325 330 335
 Ile Glu Thr Asn Glu Arg Pro Gly Thr Ile Thr Leu Gln Ala Leu Ser
 340 345 350
 Glu Ala Asn Arg Arg Leu Trp Met Glu Ala Met Asp Gly Lys Glu Pro
 355 360 365
 Ile Tyr His Ser Pro Ile Thr Lys Gln Gln Glu Met Glu Leu Asn Glu
 370 375 380
 Val Gly Phe Lys Phe Val Arg Lys Cys Ile Asn Ile Ile Glu Thr Lys
 385 390 395 400
 Gly Ile Lys Thr Glu Gly Leu Tyr Arg Thr Val Gly Ser Asn Ile Gln
 405 410 415
 Val Gln Lys Leu Leu Asn Ala Phe Phe Asp Pro Lys Cys Pro Gly Asp
 420 425 430
 Val Asp Phe His Asn Ser Asp Trp Asp Ile Lys Thr Ile Thr Ser Ser
 435 440 445
 Leu Lys Phe Tyr Leu Arg Asn Leu Ser Glu Pro Val Met Thr Tyr Arg
 450 455 460
 Leu His Lys Glu Leu Val Ser Ala Ala Lys Ser Asp Asn Leu Asp Tyr
 465 470 475 480
 Arg Leu Gly Ala Ile His Ser Leu Val Tyr Lys Leu Pro Glu Lys Asn
 485 490 495
 Arg Glu Met Leu Glu Leu Leu Ile Arg His Leu Val Asn Val Cys Glu
 500 505 510

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His Ser Lys Glu Asn Leu Met Thr Pro Ser Asn Met Gly Val Ile Phe
 515 520 525
 Gly Pro Thr Leu Met Arg Ala Gln Glu Asp Thr Val Ala Ala Met Met
 530 535 540
 Asn Ile Lys Phe Gln Asn Ile Val Val Glu Ile Leu Ile Glu His Phe
 545 550 555 560
 Gly Lys Ile Tyr Leu Gly Pro Pro Glu Glu Ser Ala Ala Pro Pro Val
 565 570 575
 Pro Pro Pro Arg Val Thr Ala Arg Arg His Lys Pro Ile Thr Ile Ser
 580 585 590
 Lys Arg Leu Leu Arg Glu Arg Thr Val Phe Tyr Thr Ser Ser Leu Asp
 595 600 605
 Glu Ser Glu Asp Glu Ile Gln His Gln Thr Pro Asn Gly Thr Ile Thr
 610 615 620
 Ser Ser Ile Glu Pro Pro Lys Pro Pro Gln His Pro Lys Leu Pro Ile
 625 630 635 640
 Gln Arg Ser Gly Glu Thr Asp Pro Gly Arg Lys Ser Pro Ser Arg Pro
 645 650 655
 Ile Leu Asp Gly Lys Leu Glu Pro Cys Pro Glu Val Asp Val Gly Lys
 660 665 670
 Leu Val Ser Arg Leu Gln Asp Gly Gly Thr Lys Ile Thr Pro Lys Ala
 675 680 685
 Thr Asn Gly Pro Met Pro Gly Ser Gly Pro Thr Lys Thr Pro Ser Phe
 690 695 700
 His Ile Lys Arg Pro Ala Pro Arg Pro Leu Ala His His Lys Glu Gly
 705 710 715 720
 Asp Ala Asp Ser Phe Ser Lys Val Arg Pro Pro Gly Glu Lys Pro Thr
 725 730 735
 Ile Ile Arg Pro Pro Val Arg Pro Pro Asp Pro Pro Cys Arg Ala Ala
 740 745 750
 Thr Pro Gln Lys Pro Glu Pro Lys Pro Asp Ile Val Ala Gly Asn Ala
 755 760 765
 Gly Glu Ile Thr Ser Ser Val Val Ala Ser Arg Thr Arg Phe Phe Glu
 770 775 780
 Thr Ala Ser Arg Lys Thr Gly Ser Ser Gln Gly Arg Leu Pro Gly Asp
 785 790 795 800
 Glu Ser

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